Kay Nieselt

List of Publications by Year
in descending order

84 papers	4,842 citations	117625 34 h-index	106344 65 g-index
93 all docs	93 docs citations	93 times ranked	7741 citing authors

#	Article	IF	Citations
1	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. Nature, 2014, 514, 494-497.	27.8	506
2	Genome-Wide Comparison of Medieval and Modern <i>Mycobacterium leprae</i>. Science, 2013, 341, 179-183.	12.6	313
3	EAGER: efficient ancient genome reconstruction. Genome Biology, 2016, 17, 60.	8.8	305
4	Global Transcriptional Start Site Mapping Using Differential RNA Sequencing Reveals Novel Antisense RNAs in Escherichia coli. Journal of Bacteriology, 2015, 197, 18-28.	2.2	287
5	High-Resolution Transcriptome Maps Reveal Strain-Specific Regulatory Features of Multiple Campylobacter jejuni Isolates. PLoS Genetics, 2013, 9, e1003495.	3.5	260
6	Progression-Specific Genes Identified by Expression Profiling of Matched Ductal Carcinomas <i>In situ</i> and Invasive Breast Tumors, Combining Laser Capture Microdissection and Oligonucleotide Microarray Analysis. Cancer Research, 2006, 66, 5278-5286.	0.9	224
7	The dynamic architecture of the metabolic switch in Streptomyces coelicolor. BMC Genomics, 2010, 11, 10.	2.8	171
8	18F-FDG-PET/CT to Select Patients with Peritoneal Carcinomatosis for Cytoreductive Surgery and Hyperthermic Intraperitoneal Chemotherapy. Annals of Surgical Oncology, 2009, 16, 1295-1303.	1.5	141
9	Origin of modern syphilis and emergence of a pandemic Treponema pallidum cluster. Nature Microbiology, 2017, 2, 16245.	13.3	138
10	Insight into the evolution and origin of leprosy bacilli from the genome sequence of <i>Mycobacterium lepromatosis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4459-4464.	7.1	134
11	Ancient Egyptian mummy genomes suggest an increase of Sub-Saharan African ancestry in post-Roman periods. Nature Communications, 2017, 8, 15694.	12.8	131
12	Phosphoglycerate kinase 1 a promoting enzyme for peritoneal dissemination in gastric cancer. International Journal of Cancer, 2010, 126, 1513-1520.	5.1	121
13	Mayday - integrative analytics for expression data. BMC Bioinformatics, 2010, 11, 121.	2.6	102
14	Aureo Wiki Ìµ The repository of the Staphylococcus aureus research and annotation community. International Journal of Medical Microbiology, 2018, 308, 558-568.	3.6	99
15	Ancient genomes reveal a high diversity of Mycobacterium leprae in medieval Europe. PLoS Pathogens, 2018, 14, e1006997.	4.7	98
16	A Novel Point Mutation Promotes Growth Phase-Dependent Daptomycin Tolerance in Staphylococcus aureus. Antimicrobial Agents and Chemotherapy, 2015, 59, 5366-5376.	3.2	90
17	Chromatin modifications induced by PML-RARÎ± repress critical targets in leukemogenesis as analyzed by ChIP-Chip. Blood, 2008, 111, 2887-2895.	1.4	73
18	PGK1 a Potential Marker for Peritoneal Dissemination in Gastric Cancer. Cellular Physiology and Biochemistry, 2008, 21, 429-436.	1.6	63

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19	cDNA microarray analysis reveals novel candidate genes expressed in human peripheral blood following exhaustive exercise. Physiological Genomics, 2005, 23, 287-294.	2.3	61
20	Mycobacterium leprae genomes from a British medieval leprosy hospital: towards understanding an ancient epidemic. BMC Genomics, 2014, 15, 270.	2.8	60
21	Identification of a novel mouse Iroquois homeobox gene,Irx5, and chromosomal localisation of all members of the mouse Iroquois gene family. , 2000, 218, 160-174.		57
22	Molecular characterization of Treponema pallidum subsp. pallidum in Switzerland and France with a new multilocus sequence typing scheme. PLoS ONE, 2018, 13, e0200773.	2.5	55
23	Metabolic Switches and Adaptations Deduced from the Proteomes of Streptomyces coelicolor Wild Type and phoP Mutant Grown in Batch Culture. Molecular and Cellular Proteomics, 2012, 11, M111.013797.	3.8	54
24	Noncoding RNA of Glutamine Synthetase I Modulates Antibiotic Production in<i>Streptomyces coelicolor</i>A3(2). Journal of Bacteriology, 2010, 192, 1160-1164.	2.2	49
25	Mayday-a microarray data analysis workbench. Bioinformatics, 2006, 22, 1010-1012.	4.1	47
26	Differential RNA-seq (dRNA-seq) for annotation of transcriptional start sites and small RNAs in Helicobacter pylori. Methods, 2015, 86, 89-101.	3.8	47
27	Transcriptomic studies of phosphate control of primary and secondary metabolism in Streptomyces coelicolor. Applied Microbiology and Biotechnology, 2012, 95, 61-75.	3.6	45
28	Low Osteogenic Differentiation Potential of Placenta-Derived Mesenchymal Stromal Cells Correlates with Low Expression of the Transcription Factors Runx2 and Twist2. Stem Cells and Development, 2013, 22, 2859-2872.	2.1	42
29	A Whole-Genome Microarray Study of<i>Arabidopsis thaliana</i>Semisolid Callus Cultures Exposed to Microgravity and Nonmicrogravity Related Spaceflight Conditions for 5 Days on Board of Shenzhou 8. BioMed Research International, 2015, 2015, 1-15.	1.9	42
30	DamageProfiler: fast damage pattern calculation for ancient DNA. Bioinformatics, 2021, 37, 3652-3653.	4.1	42
31	Phosphoglycerate Kinase 1 Promoting Tumor Progression and Metastasis in Gastric Cancer - Detected in a Tumor Mouse Model Using Positron Emission Tomography/Magnetic Resonance Imaging. Cellular Physiology and Biochemistry, 2010, 26, 147-154.	1.6	40
32	nocoRNAc: Characterization of non-coding RNAs in prokaryotes. BMC Bioinformatics, 2011, 12, 40.	2.6	39
33	Parallel detection of ancient pathogens via array-based DNA capture. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130375.	4.0	38
34	Lactate modulates gene expression in human mesenchymal stem cells. Langenbeck's Archives of Surgery, 2008, 393, 297-301.	1.9	37
35	Circadian Expression of Clock- and Tumor Suppressor Genes in Human Oral Mucosa. Cellular Physiology and Biochemistry, 2010, 26, 155-166.	1.6	36
36	DIALIGN P: fast pair-wise and multiple sequence alignment using parallel processors. BMC Bioinformatics, 2004, 5, 128.	2.6	35

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37	The PII protein GlnK is a pleiotropic regulator for morphological differentiation and secondary metabolism in Streptomyces coelicolor. Applied Microbiology and Biotechnology, 2011, 92, 1219-1236.	3.6	34
38	Yersinia pestis: New Evidence for an Old Infection. PLoS ONE, 2012, 7, e49803.	2.5	33
39	Characterization of a *mazEF* Toxin-Antitoxin Homologue from Staphylococcus equorum. Journal of Bacteriology, 2013, 195, 115-125.	2.2	33
40	Basement Membrane Remodeling in Skeletal Muscles of Patients with Limb Ischemia Involves Regulation of Matrix Metalloproteinases and Tissue Inhibitor of Matrix Metalloproteinases. Journal of Vascular Research, 2007, 44, 202-213.	1.4	32
41	Comparative analysis of structured RNAs in S. cerevisiae indicates a multitude of different functions. BMC Biology, 2007, 5, 25.	3.8	32
42	Trace amines produced by skin bacteria accelerate wound healing in mice. Communications Biology, 2020, 3, 277.	4.4	32
43	Fast and simple protein-alignment-guided assembly of orthologous gene families from microbiome sequencing reads. Microbiome, 2017, 5, 11.	11.1	31
44	Enzyme-Constrained Models and Omics Analysis of Streptomyces coelicolor Reveal Metabolic Changes that Enhance Heterologous Production. IScience, 2020, 23, 101525.	4.1	30
45	Phylogeny of the Staphylococcal Major Autolysin and Its Use in Genus and Species Typing. Journal of Bacteriology, 2012, 194, 2630-2636.	2.2	29
46	2000-year-old pathogen genomes reconstructed from metagenomic analysis of Egyptian mummified individuals. BMC Biology, 2020, 18, 108.	3.8	29
47	Open reading frames provide a rich pool of potential natural antisense transcripts in fungal genomes. Nucleic Acids Research, 2005, 33, 5034-5044.	14.5	22
48	Altering gene expression by aminocoumarins: the role of DNA supercoiling in Staphylococcus aureus. BMC Genomics, 2014, 15, 291.	2.8	22
49	Metabolic and transcriptional activities of Staphylococcus aureus challenged with high-doses of daptomycin. International Journal of Medical Microbiology, 2014, 304, 931-940.	3.6	22
50	Pan-Tetris: an interactive visualisation for Pan-genomes. BMC Bioinformatics, 2015, 16, S3.	2.6	22
51	MpsAB is important for Staphylococcus aureus virulence and growth at atmospheric CO_2 levels. Nature Communications, 2019, 10, 3627.	12.8	22
52	A Framework for Visualization of Microarray Data and Integrated Meta Information. Information Visualization, 2005, 4, 164-175.	1.9	19
53	Belowground fungal community diversity and composition associated with Norway spruce along an altitudinal gradient. PLoS ONE, 2018, 13, e0208493.	2.5	19
54	Emergence of Coding and its Specificity as a Physico-Informatic Problem. Origins of Life and Evolution of Biospheres, 2015, 45, 249-255.	1.9	18

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55	Semantic segmentation of cerebrospinal fluid and brain volume with a convolutional neural network in pediatric hydrocephalus—transfer learning from existing algorithms. Acta Neurochirurgica, 2020, 162, 2463-2474.	1.7	18
56	Mayday SeaSight: Combined Analysis of Deep Sequencing and Microarray Data. PLoS ONE, 2011, 6, e16345.	2.5	17
57	iHAT: interactive Hierarchical Aggregation Table for Genetic Association Data. BMC Bioinformatics, 2012, 13, S2.	2.6	16
58	Evolutionary Processes in the Emergence and Recent Spread of the Syphilis Agent, *Treponema pallidum*. Molecular Biology and Evolution, 2022, 39, .	8.9	16
59	Improving ancient DNA genome assembly. PeerJ, 2017, 5, e3126.	2.0	15
60	Graphs in sequence spaces: a review of statistical geometry. Biophysical Chemistry, 1997, 66, 111-131.	2.8	14
61	dRNA-seq transcriptional profiling of the FK506 biosynthetic gene cluster in *Streptomyces tsukubaensis* NRRL18488 and general analysis of the transcriptome. RNA Biology, 2017, 14, 1617-1626.	3.1	14
62	SpRay: A visual analytics approach for gene expression data. , 2009, , .		13
63	MGV: a generic graph viewer for comparative omics data. Bioinformatics, 2011, 27, 2248-2255.	4.1	13
64	Bone marrow-derived mesenchymal stromal cells differ in their attachment to fibronectin-derived peptides from term placenta-derived mesenchymal stromal cells. Stem Cell Research and Therapy, 2016, 7, 29.	5.5	13
65	The Genome of Staphylococcus epidermidis O47. Frontiers in Microbiology, 2020, 11, 2061.	3.5	13
66	Inferring genetic origins and phenotypic traits of George Bähr, the architect of the Dresden Frauenkirche. Scientific Reports, 2018, 8, 2115.	3.3	11
67	An eQTL biological data visualization challenge and approaches from the visualization community. BMC Bioinformatics, 2012, 13, S8.	2.6	9
68	inPHAP: Interactive visualization of genotype and phased haplotype data. BMC Bioinformatics, 2014, 15, 200.	2.6	9
69	The Ancient Operational Code is Embedded in the Amino Acid Substitution Matrix and aaRS Phylogenies. Journal of Molecular Evolution, 2020, 88, 136-150.	1.8	9
70	The Neuromodulator-Encoding sadA Gene Is Widely Distributed in the Human Skin Microbiome. Frontiers in Microbiology, 2020, 11, 573679.	3.5	9
71	Integrative systems biology visualization with MAYDAY. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	9
72	On the maximal cliques in c-max-tolerance graphs and their application in clustering molecular sequences. Algorithms for Molecular Biology, 2006, 1, 9.	1.2	7

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73	Reanalysis of Chinese Treponema pallidum samples: all Chinese samples cluster with SS14-like group of syphilis-causing treponemes. BMC Research Notes, 2018, 11, 16.	1.4	6
74	Differential transcriptome analysis of enterohemorrhagic Escherichia coli strains reveals differences in response to plant-derived compounds. BMC Microbiology, 2019, 19, 212.	3.3	6
75	Visualizing dimensionality reduction of systems biology data. Data Mining and Knowledge Discovery, 2013, 27, 146-165.	3.7	5
76	Expression of Desmoglein 2, Desmocollin 3 and Plakophilin 2 in Placenta and Bone Marrow-Derived Mesenchymal Stromal Cells. Stem Cell Reviews and Reports, 2017, 13, 258-266.	5.6	5
77	Secondary Metabolite Transcriptomic Pipeline (SeMa-Trap), an expression-based exploration tool for increased secondary metabolite production in bacteria. Nucleic Acids Research, 2022, 50, W682-W689.	14.5	5
78	TIALA &#x2014; Time series alignment analysis. , 2011, , .		4
79	The Draft Whole-Genome Sequence of the Antibiotic Producer Empedobacter haloabium ATCC 31962 Provides Indications for Its Taxonomic Reclassification. Microbiology Resource Announcements, 2019, 8, .	0.6	4
80	DACCORâ€"Detection, characterization, and reconstruction of repetitive regions in bacterial genomes. PeerJ, 2018, 6, e4742.	2.0	3
81	iHAT: Interactive hierarchical aggregation table. , 2011, , .		2
82	Draft Genome Sequence of <i>Ochrobactrum</i> sp. Strain MC-1LL, a Bacterial Strain with Antimicrobial Properties, Isolated from Marine Sediments in Nigeria. Microbiology Resource Announcements, 2020, 9, .	0.6	2
83	REVEAL--visual eQTL analytics. Bioinformatics, 2012, 28, i542-i548.	4.1	0
84	Non-coding RNA, Prediction. , 2013, , 1534-1538.		0